

A. Kubelik

Re-run



#5

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/047,593

DATE: 12/06/2002

TIME: 17:44:19

Input Set : A:\PTO.AMC.txt

Output Set: N:\CRF4\12062002\J047593.raw

4 <110> APPLICANT: Crane, Edmund H. III  
5 Rice, Douglas A.  
7 <120> TITLE OF INVENTION: Maize NPR1 Polynucleotides and Methods  
8 of Use  
10 <130> FILE REFERENCE: 1090D2  
C--> 12 <140> CURRENT APPLICATION NUMBER: US/10/047,593  
C--> 12 <141> CURRENT FILING DATE: 2002-01-15  
12 <150> PRIOR APPLICATION NUMBER: 60/130,692  
13 <151> PRIOR FILING DATE: 1999-04-23  
15 <150> PRIOR APPLICATION NUMBER: 09/551,778  
16 <151> PRIOR FILING DATE: 2000-04-18  
18 <160> NUMBER OF SEQ ID NOS: 6  
20 <170> SOFTWARE: FastSEQ for Windows Version 4.0  
22 <210> SEQ ID NO: 1  
23 <211> LENGTH: 2154  
24 <212> TYPE: DNA  
25 <213> ORGANISM: Zea mays  
27 <220> FEATURE:  
28 <221> NAME/KEY: CDS  
29 <222> LOCATION: (67)...(1929)  
31 <221> NAME/KEY: 3'UTR  
32 <222> LOCATION: (1933)...(2154)  
W--> 34 <221> 5'UTR  
35 <222> LOCATION: (1)...(66)  
W--> 37 <400> 1  
38 gtcgtagtgg tccgggtccg gcacaagtag gggctcgcgt cttgcgcttg gcagttgtgg 60  
39 gaagcc atg gag ccg tcg tcg tcc atc acg ttc gcg tcg tcg tcg tcg 108  
40 Met Glu Pro Ser Ser Ser Ile Thr Phe Ala Ser Ser Ser Ser  
41 1 5 10  
43 tac ctg tcc aac ggc tcg agc ccc tgt tcc gtc gcg ctg ccg ccg cca 156  
44 Tyr Leu Ser Asn Gly Ser Ser Pro Cys Ser Val Ala Leu Pro Pro Pro  
45 15 20 25 30  
47 ggg ccg ccc cag act ccc ccg ttg cct gcc ggc cag ggg tgg ggt ggt 204  
48 Gly Pro Pro Gln Thr Pro Pro Leu Pro Ala Gly Gln Gly Trp Gly Gly  
49 35 40 45  
51 gga gtc gct gcc gca ggg agc gga ggc agc gtg gag gcc gtg agc ctg 252  
52 Gly Val Ala Ala Ala Gly Ser Gly Gly Ser Val Glu Ala Val Ser Leu  
53 50 55 60  
55 aac ccg ctc agc aaa aac ctc gag ccg ctg ctc ctc gac ccg gac cta 300  
56 Asn Arg Leu Ser Lys Asn Leu Glu Arg Leu Leu Leu Asp Pro Asp Leu  
57 65 70 75  
59 gac tgc agc gac gcc gac gtc gat gtg ccc gac ggt ggg ccg ccc gta 348  
60 Asp Cys Ser Asp Ala Asp Val Asp Val Pro Asp Gly Gly Pro Pro Val

ENTERED

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61	80	85	90	
63	ccc atc cac cgc tgc atc ctt gcc gca cgc agc gac ttc ttc tac gac	396		
64	Pro Ile His Arg Cys Ile Leu Ala Ala Arg Ser Asp Phe Phe Tyr Asp			
65	95 100 105 110			
67	ctc ttc gcc gct cgc ggc cgc gca ggg gca gcg cgc ggt gat gcg gcc	444		
68	Leu Phe Ala Ala Arg Gly Arg Ala Gly Ala Ala Arg Gly Asp Ala Ala			
69	115 120 125			
71	gcc ggc gcc gga gta gcc gcg gag ggg gct gcc agt gga agg ccg ccg	492		
72	Ala Gly Ala Gly Val Ala Ala Glu Gly Ala Ala Ser Gly Arg Pro Arg			
73	130 135 140			
75	tac aag atg gag gat ctc gtt ccc gcc ggc cgc gtg ggg cgc gag gcc	540		
76	Tyr Lys Met Glu Asp Leu Val Pro Ala Gly Arg Val Gly Arg Glu Ala			
77	145 150 155			
79	ttc cag gcg ttt ctg ggg tac ctg tac acc ggc aag ctc ccg ccg gca	588		
80	Phe Gln Ala Phe Leu Gly Tyr Leu Tyr Thr Gly Lys Leu Arg Pro Ala			
81	160 165 170			
83	ccg gtc gac gtg gtg tct tgt gct gac cca gtg tgc cat cac gat tcg	636		
84	Pro Val Asp Val Val Ser Cys Ala Asp Pro Val Cys His His Asp Ser			
85	175 180 185 190			
87	tgc ccg ccg gcc atc agg tcc gcg gtc gag ctc atg tac gcg gcg tgt	684		
88	Cys Pro Pro Ala Ile Arg Ser Ala Val Glu Leu Met Tyr Ala Ala Cys			
89	195 200 205			
91	acc ttc aag atc ccc gag ctc acc tcg ctc ttc cag cgc ccg ctt ctt	732		
92	Thr Phe Lys Ile Pro Glu Leu Thr Ser Leu Phe Gln Arg Arg Leu Leu			
93	210 215 220			
95	aat ttt gta gac aag act cta gtg gag gat gtt att cct att ctg gaa	780		
96	Asn Phe Val Asp Lys Thr Leu Val Glu Asp Val Ile Pro Ile Leu Glu			
97	225 230 235			
99	gtt gct tcc cac tca ggg ctg act caa gtg atc gac aaa tgt att caa	828		
100	Val Ala Ser His Ser Gly Leu Thr Gln Val Ile Asp Lys Cys Ile Gln			
101	240 245 250			
103	agg att gct aga tca gat ctc gac gat ata tct ttg gat aag gag ctc	876		
104	Arg Ile Ala Arg Ser Asp Leu Asp Asp Ile Ser Leu Asp Lys Glu Leu			
105	255 260 265 270			
107	cct cca gaa gca gtt gat gag ata aaa aat ttg cgc aag aag tca caa	924		
108	Pro Pro Glu Ala Val Asp Glu Ile Lys Asn Leu Arg Lys Lys Ser Gln			
109	275 280 285			
111	act gct gat ggt gat acg ttc att tcg gac cct gtg cat gag aaa aga	972		
112	Thr Ala Asp Gly Asp Thr Phe Ile Ser Asp Pro Val His Glu Lys Arg			
113	290 295 300			
115	gtc aga aga atc cac agg gca ctt gac tct gat gat gtt gag ctt gtg	1020		
116	Val Arg Arg Ile His Arg Ala Leu Asp Ser Asp Asp Val Glu Leu Val			
117	305 310 315			
119	aag ttg ctt ctt aat gag tcc gac atc aca tta gat gat gcc aac gca	1068		
120	Lys Leu Leu Leu Asn Glu Ser Asp Ile Thr Leu Asp Asp Ala Asn Ala			
121	320 325 330			
123	tta cac tat gct gct tct tac tgt gat cct aaa gtt gtc tca gag ctg	1116		
124	Leu His Tyr Ala Ala Ser Tyr Cys Asp Pro Lys Val Val Ser Glu Leu			
125	335 340 345 350			

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127	tta gat ttg gca atg gct aac tta aat ttg aag aat agc cgt ggg tac	1164
128	Leu Asp Leu Ala Met Ala Asn Leu Asn Leu Lys Asn Ser Arg Gly Tyr	
129	355 360 365	
131	aca gca ctc cac ttg gct gct atg agg aga gaa cca gct ata atc atg	1212
132	Thr Ala Leu His Leu Ala Ala Met Arg Arg Glu Pro Ala Ile Ile Met	
133	370 375 380	
135	tgt ctc ctt aac aaa ggg gca aat gtg tca caa ctg aca gct gat ggc	1260
136	Cys Leu Leu Asn Lys Gly Ala Asn Val Ser Gln Leu Thr Ala Asp Gly	
137	385 390 395	
139	agg agc gca att ggt att tgt cgg agg tta aca aga gca aaa gac tac	1308
140	Arg Ser Ala Ile Gly Ile Cys Arg Arg Leu Thr Arg Ala Lys Asp Tyr	
141	400 405 410	
143	aat aca aag atg gag cag ggt caa gaa tca aat aaa gat agg ctg tgt	1356
144	Asn Thr Lys Met Glu Gln Gly Gln Glu Ser Asn Lys Asp Arg Leu Cys	
145	415 420 425 430	
147	ata gat att cta gag agg gag atg atg cgg aat cct atg gcg gtg gaa	1404
148	Ile Asp Ile Leu Glu Arg Glu Met Met Arg Asn Pro Met Ala Val Glu	
149	435 440 445	
151	gat gcc gtc acc tcg cct ttg ttg gca gat gat ctt cac atg aag ctt	1452
152	Asp Ala Val Thr Ser Pro Leu Leu Ala Asp Asp Leu His Met Lys Leu	
153	450 455 460	
155	ctc tac ctg gaa aac aga gtt gca ttt gct aga ttg ttc ttt cct gct	1500
156	Leu Tyr Leu Glu Asn Arg Val Ala Phe Ala Arg Leu Phe Phe Pro Ala	
157	465 470 475	
159	gaa gcc aag gtc gcc atg caa atc gca caa gca gac acc aca gaa gaa	1548
160	Glu Ala Lys Val Ala Met Gln Ile Ala Gln Ala Asp Thr Thr Glu Glu	
161	480 485 490	
163	ttc ggc ggt ata gtt gca gtt gca gca agc act tct ggt aaa ctg agg	1596
164	Phe Gly Gly Ile Val Ala Val Ala Ala Ser Thr Ser Gly Lys Leu Arg	
165	495 500 505 510	
167	gag gtg gac ctt aat gag acg cca gtg aca caa aac aaa agg ctc cgt	1644
168	Glu Val Asp Leu Asn Glu Thr Pro Val Thr Gln Asn Lys Arg Leu Arg	
169	515 520 525	
171	tca agg gta gat gca ctg atg aaa aca gtg gag ctg ggc cgt cgg tac	1692
172	Ser Arg Val Asp Ala Leu Met Lys Thr Val Glu Leu Gly Arg Arg Tyr	
173	530 535 540	
175	ttc ccg aac tgc tcg cag gtg ctg gac aag ttc ctg gag gac gat ctg	1740
176	Phe Pro Asn Cys Ser Gln Val Leu Asp Lys Phe Leu Glu Asp Asp Leu	
177	545 550 555	
179	ccg gaa ggt ctg gac cag ttc tac ctc cag agg ggc aca gcc gat gag	1788
180	Pro Glu Gly Leu Asp Gln Phe Tyr Leu Gln Arg Gly Thr Ala Asp Glu	
181	560 565 570	
183	cag aag gtg aag agg atg cgc ttc tgc gag ctg aaa gag gac gtg ctg	1836
184	Gln Lys Val Lys Arg Met Arg Phe Cys Glu Leu Lys Glu Asp Val Leu	
185	575 580 585 590	
187	aag gcg ttt agc aag gac aag gcg gag ggc agc gtg ttc tcg ggc ctg	1884
188	Lys Ala Phe Ser Lys Asp Lys Ala Glu Gly Ser Val Phe Ser Gly Leu	
189	595 600 605	
191	tcc tcg tcg tcg tcg tgc tcg ccg ccc cag aag tat gcc cag agg	1929

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192 Ser Ser Ser Ser Ser Cys Ser Pro Pro Gln Lys Tyr Ala Gln Arg
193          610          615          620
195 tgatcaaggc accagttttt gccgtatagt ttgttatcat ggtcttcgag acttggaccc 1989
196 ggacagcata tagggacatg tacacctgtg tatgtatagt gcttacaatt ggcgtaagta 2049
197 gaactatatg tatggaacat aaggaaacat ggcaggaaca ccgtgcaaaa agatgaaaag 2109
198 atggccgaag tgctctatgc gaaaaaaaaa aaaaaaaaaa aaaaaa 2154
200 <210> SEQ ID NO: 2
201 <211> LENGTH: 621
202 <212> TYPE: PRT
203 <213> ORGANISM: Zea mays
205 <400> SEQUENCE: 2
206 Met Glu Pro Ser Ser Ser Ile Thr Phe Ala Ser Ser Ser Ser Tyr Leu
207 1          5          10          15
208 Ser Asn Gly Ser Ser Pro Cys Ser Val Ala Leu Pro Pro Pro Gly Pro
209          20          25          30
210 Pro Gln Thr Pro Pro Leu Pro Ala Gly Gln Gly Trp Gly Gly Gly Val
211          35          40          45
212 Ala Ala Ala Gly Ser Gly Gly Ser Val Glu Ala Val Ser Leu Asn Arg
213          50          55          60
214 Leu Ser Lys Asn Leu Glu Arg Leu Leu Leu Asp Pro Asp Leu Asp Cys
215 65          70          75          80
216 Ser Asp Ala Asp Val Asp Val Pro Asp Gly Gly Pro Pro Val Pro Ile
217          85          90          95
218 His Arg Cys Ile Leu Ala Ala Arg Ser Asp Phe Phe Tyr Asp Leu Phe
219          100          105          110
220 Ala Ala Arg Gly Arg Ala Gly Ala Ala Arg Gly Asp Ala Ala Ala Gly
221          115          120          125
222 Ala Gly Val Ala Ala Glu Gly Ala Ala Ser Gly Arg Pro Arg Tyr Lys
223          130          135          140
224 Met Glu Asp Leu Val Pro Ala Gly Arg Val Gly Arg Glu Ala Phe Gln
225 145          150          155          160
226 Ala Phe Leu Gly Tyr Leu Tyr Thr Gly Lys Leu Arg Pro Ala Pro Val
227          165          170          175
228 Asp Val Val Ser Cys Ala Asp Pro Val Cys His His Asp Ser Cys Pro
229          180          185          190
230 Pro Ala Ile Arg Ser Ala Val Glu Leu Met Tyr Ala Ala Cys Thr Phe
231          195          200          205
232 Lys Ile Pro Glu Leu Thr Ser Leu Phe Gln Arg Arg Leu Leu Asn Phe
233          210          215          220
234 Val Asp Lys Thr Leu Val Glu Asp Val Ile Pro Ile Leu Glu Val Ala
235 225          230          235          240
236 Ser His Ser Gly Leu Thr Gln Val Ile Asp Lys Cys Ile Gln Arg Ile
237          245          250          255
238 Ala Arg Ser Asp Leu Asp Asp Ile Ser Leu Asp Lys Glu Leu Pro Pro
239          260          265          270
240 Glu Ala Val Asp Glu Ile Lys Asn Leu Arg Lys Lys Ser Gln Thr Ala
241          275          280          285
242 Asp Gly Asp Thr Phe Ile Ser Asp Pro Val His Glu Lys Arg Val Arg
243          290          295          300

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```

244 Arg Ile His Arg Ala Leu Asp Ser Asp Asp Val Glu Leu Val Lys Leu
245 305          310          315          320
246 Leu Leu Asn Glu Ser Asp Ile Thr Leu Asp Asp Ala Asn Ala Leu His
247          325          330          335
248 Tyr Ala Ala Ser Tyr Cys Asp Pro Lys Val Val Ser Glu Leu Leu Asp
249          340          345          350
250 Leu Ala Met Ala Asn Leu Asn Leu Lys Asn Ser Arg Gly Tyr Thr Ala
251          355          360          365
252 Leu His Leu Ala Ala Met Arg Arg Glu Pro Ala Ile Ile Met Cys Leu
253 370          375          380
254 Leu Asn Lys Gly Ala Asn Val Ser Gln Leu Thr Ala Asp Gly Arg Ser
255 385          390          395          400
256 Ala Ile Gly Ile Cys Arg Arg Leu Thr Arg Ala Lys Asp Tyr Asn Thr
257          405          410          415
258 Lys Met Glu Gln Gly Gln Glu Ser Asn Lys Asp Arg Leu Cys Ile Asp
259          420          425          430
260 Ile Leu Glu Arg Glu Met Met Arg Asn Pro Met Ala Val Glu Asp Ala
261          435          440          445
262 Val Thr Ser Pro Leu Leu Ala Asp Asp Leu His Met Lys Leu Leu Tyr
263 450          455          460
264 Leu Glu Asn Arg Val Ala Phe Ala Arg Leu Phe Phe Pro Ala Glu Ala
265 465          470          475          480
266 Lys Val Ala Met Gln Ile Ala Gln Ala Asp Thr Thr Glu Glu Phe Gly
267          485          490          495
268 Gly Ile Val Ala Val Ala Ala Ser Thr Ser Gly Lys Leu Arg Glu Val
269          500          505          510
270 Asp Leu Asn Glu Thr Pro Val Thr Gln Asn Lys Arg Leu Arg Ser Arg
271          515          520          525
272 Val Asp Ala Leu Met Lys Thr Val Glu Leu Gly Arg Arg Tyr Phe Pro
273 530          535          540
274 Asn Cys Ser Gln Val Leu Asp Lys Phe Leu Glu Asp Asp Leu Pro Glu
275 545          550          555          560
276 Gly Leu Asp Gln Phe Tyr Leu Gln Arg Gly Thr Ala Asp Glu Gln Lys
277          565          570          575
278 Val Lys Arg Met Arg Phe Cys Glu Leu Lys Glu Asp Val Leu Lys Ala
279          580          585          590
281 Phe Ser Lys Asp Lys Ala Glu Gly Ser Val Phe Ser Gly Leu Ser Ser
283          595          600          605
285 Ser Ser Ser Cys Ser Pro Pro Gln Lys Tyr Ala Gln Arg
287 610          615          620
288 <210> SEQ ID NO: 3
289 <211> LENGTH: 7789
290 <212> TYPE: DNA
291 <213> ORGANISM: Zea mays
293 <220> FEATURE:
294 <221> NAME/KEY: promoter
295 <222> LOCATION: (1)...(2715)
297 <221> NAME/KEY: 5'UTR
298 <222> LOCATION: (2716)...(2781)

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## VERIFICATION SUMMARY

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L:12 M:270 C: Current Application Number differs, Replaced Current Application No  
L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
L:34 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:1  
L:37 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:1  
L:300 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:3  
L:303 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:3  
L:306 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:3  
L:309 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:3  
L:312 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:3  
L:315 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:3  
L:318 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:3  
L:321 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:3  
L:324 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:3